

W/1012

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/963,285

DATE: 10/10/2001

TIME: 14:02:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\10102001\I963285.raw

4 <110> APPLICANT: Enerbck, Sven
 5 Krook, Katarina
 6 Rondahl, Lena
 7 Wasserman, Wyeth
 9 <120> TITLE OF INVENTION: PROMOTER SEQUENCES
 11 <130> FILE REFERENCE: 13425-042001
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/963,285 *OK*
 C--> 13 <141> CURRENT FILING DATE: 2001-09-26
 13 <150> PRIOR APPLICATION NUMBER: SE 0004102-0
 14 <151> PRIOR FILING DATE: 2000-11-09
 16 <150> PRIOR APPLICATION NUMBER: US 60/238,897
 17 <151> PRIOR FILING DATE: 2000-10-10
 19 <150> PRIOR APPLICATION NUMBER: SE 0003435-5
 20 <151> PRIOR FILING DATE: 2000-09-26
 22 <160> NUMBER OF SEQ ID NOS: 24
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 6458
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (2235)...(3737)
 35 <400> SEQUENCE: 1

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37	cttttattgg	aaataagtgg	cacgccccat	tgcctctag	tcgcctcccc	gaagcgaaga	120
38	ggccgaagcg	aagaggcctg	gtgggttgtc	tcaacatcc	tttgctgaga	atcgaatacg	180
39	cagccatga	acagccagga	agggtcaag	gaaacctgaa	atacaaatgt	tctccctgaa	240
40	gccctttcc	ctgcccacc	agaccagcaa	cttccaaaat	tctgcccgt	tttagccttg	300
41	ttaaagggtt	gtctcactcc	ttcagggaaa	gtggggaaag	gggatctgt	tattgaggtg	360
42	tgaaggaat	aaataatcg	tccacaaata	aacaaactgt	ccgggattcc	tagagggaaag	420
43	gagaaatcct	tgaaggagat	ccaagtcgct	ccaggtctgc	ctgccgaata	atatcatccc	480
44	gaaggatct	tgaaccgtt	gcaatcaacc	gctcacccag	tctccacag	gagcgcgc	540
45	cctaactcac	cctaccacc	caacaaaaca	aaaaaaaggc	tgaaatatacg	aaaagcaact	600
46	tggggctcc	cagggggacg	ttgccaggag	caggaggcag	ggacagcgcc	ctagggtcgg	660
47	tgttagcggc	cggccggcgc	ctggccacg	ggaaacgtcc	acgcttggt	ccgcgggtgc	720
48	gccccgcgtca	ttgcgcgcgc	cttcgagcca	agccccgcgc	gaaaacaggc	tcgggtttct	780
49	cctcgcagg	cccaggaact	cggctctgcc	tggccgggt	gggtcgctgc	attgtcccg	840
50	tcttctggga	gtgcggggtc	agcttggta	agggaaatttc	tacctggaa	aaggagacg	900
51	agttcgaag	ctgaagtgg	taggctgcg	gtgtccacgc	gggagacgaa	agggggaaat	960
52	agcagagtca	tttcaccctt	ttccccaaac	cccacaaaac	tgctcgacgc	gacgcggatg	1020
53	atctaccgaa	ttcccccgca	attcgagga	ttaagttgtc	agttagcgcac	ttgtctacctt	1080
54	ccctctatg	caactccgctg	cctggctcc	cggcggggag	cgagggaaac	tcagttgt	1140
55	gggttacct	ctaaaacctc	gataggttat	ccttgacgac	cccgagcctg	gaaactccct	1200
56	gttgatgatt	aattatttga	ttaaataagt	ataacatcca	ggagaggccc	tgccattcca	1260
57	atccagcgcg	tttgcttttg	aatccattac	acctggggcc	ccataattag	gaaatcta	1320
58	tattcgcttc	atcactcatt	aataagaaaa	atgtcccagg	atcattgtca	cttacaaggt	1380

ENTERED

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59	cttgggaga	gatattttac	tctattaatc	cattctattt	tatatttcaa	attgattttt	1440											
60	ttaacagag	gaaagtggct	atctttttgt	tttggcatt	tgcccatt	cacccaaatg	1500											
61	tgtcataaa	ataaattta	ataagatata	acttttaaa	aagtttcaa	gtgaagacgg	1560											
62	agtcgcgcg	gaggccggg	cgcggggtc	ttagagccga	cggattcccg	cgctccctcgc	1620											
63	ccgattggc	gccggactcc	tctcagctgc	cgggttattt	gctcaaagt	ccggaggggg	1680											
64	gcgtggcccg	aggaaagtaa	aaactcgctt	tcagcaagaa	gacttttga	actttccca	1740											
65	atccctaaaa	gggacttggc	ctcttttct	gggctcagcg	gggcagccgc	tcggaccccg	1800											
66	gcgcgctgac	cctcgggct	gccgattcgc	tggggcttg	gagagcctcc	tgcggccctc	1860											
67	ctcgccggg	ccgagggtcc	accttggtcc	ccagggcgcg	gcgtctccgc	tgggtcccg	1920											
68	gcccccgc	tgcccgcgt	gccgcccgcg	ggtcttggag	ccagcgagga	gcggggccgg	1980											
69	cgtcgctt	gccccggg	cgcctccag	gatgcgcgatc	cgcgggttcc	gctgaaagcg	2040											
70	cgcccctg	ctcgccccga	gcgacgacga	ccgcgcaccc	tgcggcccg	ggctgccagg	2100											
71	agaccggggc	cgccccctcc	gtccccctcc	tctccccctc	tggctctc	gcgcctctc	2160											
72	gtctcaggg	ccccccctcgc	tccccccggcc	gcagttcggt	cgcgaggccg	ccggcgagcc	2220											
73	gtctcggaaag	cagc	atg	cag	gcg	cgc	1440											
74				Met	Gln	Ala	Arg	Tyr	Ser	Val	Ser	Asp	Pro	Asn	Ala			
75				1			5						10					
77	ctg	gga	gtg	gtg	ccc	tac	ctg	agc	gag	cag	aat	tac	tac	cg	gct	g	2318	
78	Leu	Gly	Val	Val	Pro	Tyr	Leu	Ser	Glu	Gln	Asn	Tyr	Tyr	Arg	Ala	Ala		
79					15				20				25					
81	ggc	agc	tac	ggc	ggc	atg	gcc	agc	ccc	atg	ggc	gtc	tat	tcc	ggc	cac	2366	
82	Gly	Ser	Tyr	Gly	Gly	Met	Ala	Ser	Pro	Met	Gly	Val	Tyr	Ser	Gly	His		
83					30				35				40					
85	ccg	gag	cag	tac	agc	g	ggg	atg	ggc	cgc	tcc	tac	g	c	cc	ta	2414	
86	Pro	Glu	Gln	Tyr	Ser	Ala	Gly	Met	Gly	Arg	Ser	Tyr	Ala	Pro	Tyr	His		
87					45				50				55			60		
89	cac	cac	cag	ccc	g	cg	g	cct	aag	gac	ctg	gt	aag	cc	cc	ta	2462	
90	His	His	Gln	Pro	Ala	Ala	Pro	Lys	Asp	Leu	Val	Lys	Pro	Pro	Tyr	Ser		
91					65					70				75				
93	tac	atc	g	ctc	atc	acc	atg	gcc	atc	cag	aa	g	cc	cc	ta	2510		
94	Tyr	Ile	Ala	Leu	Ile	Thr	Met	Ala	Ile	Gln	Asn	Ala	Pro	Glu	Lys	Lys		
95					80				85				90					
97	atc	acc	ttt	aa	g	gc	atc	tac	cag	ttt	atc	atg	g	cc	tt	cc	ttc	2558
98	Ile	Thr	Leu	Asn	Gly	Ile	Tyr	Gln	Phe	Ile	Met	Asp	Arg	Phe	Pro	Phe		
99					95				100				105					
101	tac	cg	gag	aa	ag	cag	ggc	tgg	cag	aa	gc	atc	cg	cc	ca	ct	2606	
102	Tyr	Arg	Glu	Asn	Lys	Gln	Gly	Trp	Gln	Asn	Ser	Ile	Arg	His	Asn	Leu		
103					110				115				120					
105	tcg	ctc	aa	gag	tgc	ttc	gtc	aag	gt	cc	cgc	gac	gac	aag	aa	cc	2654	
106	Ser	Leu	Asn	Glu	Cys	Phe	Val	Lys	Val	Pro	Arg	Asp	Asp	Lys	Lys	Pro		
107					125				130				135			140		
109	ggc	aag	ggc	agt	tac	tgg	acc	ctg	gac	ccg	gac	tcc	tac	aa	atg	ttc	2702	
110	Gly	Lys	Gly	Ser	Tyr	Trp	Thr	Leu	Asp	Pro	Asp	Ser	Tyr	Asn	Met	Phe		
111					145					150				155				
113	gag	aa	g	gc	agc	ttc	ctg	cg	cg	cg	cg	ttc	aaa	aa	ag	gac	2750	
114	Glu	Asn	Gly	Ser	Phe	Leu	Arg	Arg	Arg	Arg	Arg	Phe	Lys	Lys	Lys	Asp		
115					160				165				170					
117	gt	tg	tcc	aa	gag	aa	gag	gg	cg	gc	cac	ctc	aa	gag	cc	cc	cc	2798
118	Val	Ser	Lys	Glu	Lys	Glu	Glu	Arg	Ala	His	Leu	Lys	Glu	Pro	Pro	Pro		

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119	175	180	185															
121	gcg	gcg	tcc	aag	ggc	gcc	ccg	gcc	acc	ccc	cac	cta	gcg	gac	gcc	ccc	2846	
122	Ala	Ala	Ser	Lys	Gly	Ala	Pro	Ala	Thr	Pro	His	Leu	Ala	Asp	Ala	Pro		
123	190						195				200							
125	aag	gag	gcc	gag	aag	aag	gtg	gtg	atc	aag	agc	gag	gag	gag	gag	tcc	ccg	2894
126	Lys	Glu	Ala	Glu	Lys	Lys	Val	Val	Ile	Lys	Ser	Glu	Ala	Ala	Ser	Pro		
127	205						210				215					220		
129	gcg	ctg	ccg	gtc	atc	acc	aag	gtg	gag	acg	ctg	agc	ccc	gag	agc	gag	2942	
130	Ala	Leu	Pro	Val	Ile	Thr	Lys	Val	Glu	Thr	Leu	Ser	Pro	Glu	Ser	Ala		
131							225				230					235		
133	ctg	cag	ggc	agc	ccg	cgc	agc	gag	gcc	tcc	acg	ccc	gcc	ggc	tcc	ccc	2990	
134	Leu	Gln	Gly	Ser	Pro	Arg	Ser	Ala	Ala	Ser	Thr	Pro	Glu	Ser	Ala			
135							240				245					250		
137	gac	ggt	tcg	ctg	ccg	gag	cac	cac	gcc	gag	ccc	aat	ggg	ctg	cct		3038	
138	Asp	Gly	Ser	Leu	Pro	Glu	His	His	Ala	Ala	Ala	Pro	Asn	Gly	Leu	Pro		
139							255				260					265		
141	ggc	tcc	agc	gtg	gag	aac	atc	atg	acc	ctg	cga	acg	tcg	ccg	ccg	ggc	3086	
142	Gly	Phe	Ser	Val	Glu	Asn	Ile	Met	Thr	Leu	Arg	Thr	Ser	Pro	Pro	Gly		
143							270				275					280		
145	gga	gag	ctg	agc	ccg	ggg	gcc	gga	cgc	gag	ccc	ctg	gtg	gtg	ccg	ccg	3134	
146	Gly	Glu	Leu	Ser	Pro	Gly	Ala	Gly	Arg	Ala	Gly	Leu	Val	Val	Pro	Pro		
147							285				290					300		
149	ctg	gag	ctg	cca	tac	gcc	gcc	ccg	ccc	gcc	tac	ggc	cag	ccg			3182	
150	Leu	Ala	Leu	Pro	Tyr	Ala	Ala	Ala	Pro	Pro	Ala	Ala	Tyr	Gly	Gln	Pro		
151							305				310					315		
153	tgc	gct	cag	ggc	ctg	gag	gcc	ggg	gcc	ggg	ggc	tac	cag	tgc	agc		3230	
154	Cys	Ala	Gln	Gly	Leu	Glu	Ala	Gly	Ala	Ala	Gly	Gly	Tyr	Gln	Cys	Ser		
155							320				325					330		
157	atg	cga	gag	atg	agc	ctg	tac	acc	ggg	gcc	gag	cgg	ccg	gag	ccg	atg	3278	
158	Met	Arg	Ala	Met	Ser	Leu	Tyr	Thr	Gly	Ala	Glu	Arg	Pro	Ala	His	Met		
159							335				340					345		
161	tgc	gtc	ccg	ccc	gcc	ctg	gac	gag	gcc	ctc	tcg	gac	cac	ccg	agc	ggc	3326	
162	Cys	Val	Pro	Pro	Ala	Leu	Asp	Glu	Ala	Leu	Ser	Asp	His	Pro	Ser	Gly		
163							350				355					360		
165	ccc	acg	tcg	ccc	ctg	agc	gct	ctc	aac	ctc	gcc	gcc	ggc	cag	gag	ggc	3374	
166	Pro	Thr	Ser	Pro	Leu	Ser	Ala	Leu	Asn	Leu	Ala	Ala	Gly	Gln	Glu	Gly		
167							365				370					380		
169	gcg	ctc	gcc	ggc	acg	ggc	cac	cac	cac	cac	cag	ggc	cac	cac	cac		3422	
170	Ala	Leu	Ala	Ala	Thr	Gly	His	His	His	Gln	His	His	Gly	His	His	His		
171							385				390					395		
173	ccg	cag	ggc	ccg	ccc	ccg	ccg	gct	ccc	cag	ccc	cag	ccg	acg	ccg		3470	
174	Pro	Gln	Ala	Pro	Pro	Pro	Pro	Ala	Pro	Gln	Pro	Gln	Pro	Thr	Pro			
175							400				405					410		
177	cag	ccc	ggg	gcc	gcc	gag	gag	gag	gcc	tcc	tgg	tat	ctc	aac	cac		3518	
178	Gln	Pro	Gly	Ala	Ala	Ala	Gln	Ala	Ala	Ser	Trp	Tyr	Leu	Asn	His			
179							415				420					425		
181	agc	ggg	gac	ctg	aac	cac	ctc	ccc	ggc	cac	acg	tcc	gcg	gcc	cag	cag	3566	
182	Ser	Gly	Asp	Leu	Asn	His	Leu	Pro	Gly	His	Thr	Phe	Ala	Ala	Gln	Gln		
183							430				435					440		

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238	tgatggtttc	atttacttc	tgctcgcttc	atgctatttgc	ccccaggaga	agaggagagt	6037										
239	attccagacg	gtaagcgagc	tggcttttc	ccttccctag	acgttttaaa	gaaatcttc	6097										
240	tgaaagcttgc	ccctcatcg	aagcttgaa	accgttgg	tcctgttagt	ggcgagggct	6157										
241	gagagacacg	cggagaaata	aaggagagcg	acgggtgtgc	tgagagcccc	caggctctgt	6217										
242	gttggaaacta	agctgggc	ttgcacctt	aggaagcctt	tttaaagaag	tcctgctgt	6277										
243	tggggccgg	aagccaa	gagtgggc	tgtggagg	atcgggagg	gtcttacca	6337										
244	ctccttggg	aacgtggca	acgggggat	tgtatctgaa	gctttattca	ggtcttcggc	6397										
245	gycagcagag	tggagaacca	ggcccttagt	gtgtacggc	ctggggattt	tggactcat	6457										
246	C						6458										
248	<210>	SEQ ID NO: 2															
249	<211>	LENGTH: 501															
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251	<213>	ORGANISM: Homo sapiens															
253	<400>	SEQUENCE: 2															
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255	1				5				10						15		
256	Pro	Tyr	Leu	Ser	Glu	Gln	Asn	Tyr	Tyr	Arg	Ala	Ala	Gly	Ser	Tyr	Gly	
257								20		25					30		
258	Gly	Met	Ala	Ser	Pro	Met	Gly	Val	Tyr	Ser	Gly	His	Pro	Glu	Gln	Tyr	
259								35		40					45		
260	Ser	Ala	Gly	Met	Gly	Arg	Ser	Tyr	Ala	Pro	Tyr	His	His	His	Gln	Pro	
261								50		55					60		
262	Ala	Ala	Pro	Lys	Asp	Leu	Val	Lys	Pro	Pro	Tyr	Ser	Tyr	Ile	Ala	Leu	
263								65		70					75		80
264	Ile	Thr	Met	Ala	Ile	Gln	Asn	Ala	Pro	Glu	Lys	Lys	Ile	Thr	Leu	Asn	
265								85		90					95		
266	Gly	Ile	Tyr	Gln	Phe	Ile	Met	Asp	Arg	Phe	Pro	Phe	Tyr	Arg	Glu	Asn	
267								100		105					110		
268	Lys	Gln	Gly	Trp	Gln	Asn	Ser	Ile	Arg	His	Asn	Leu	Ser	Leu	Asn	Glu	
269								115		120					125		
270	Cys	Phe	Val	Lys	Val	Pro	Arg	Asp	Asp	Lys	Lys	Pro	Gly	Lys	Gly	Ser	
271								130		135					140		
272	Tyr	Trp	Thr	Leu	Asp	Pro	Asp	Ser	Tyr	Asn	Met	Phe	Glu	Asn	Gly	Ser	
273								145		150					155		160
274	Phe	Leu	Arg	Arg	Arg	Arg	Arg	Phe	Lys	Lys	Lys	Asp	Val	Ser	Lys	Glu	
275								165		170					175		
276	Lys	Glu	Glu	Arg	Ala	His	Leu	Lys	Glu	Pro	Pro	Pro	Ala	Ala	Ser	Lys	
277								180		185					190		
278	Gly	Ala	Pro	Ala	Thr	Pro	His	Leu	Ala	Asp	Ala	Pro	Lys	Glu	Ala	Glu	
279								195		200					205		
280	Lys	Lys	Val	Val	Ile	Lys	Ser	Glu	Ala	Ala	Ser	Pro	Ala	Leu	Pro	Val	
281								210		215					220		
282	Ile	Thr	Lys	Val	Glu	Thr	Leu	Ser	Pro	Glu	Ser	Ala	Leu	Gln	Gly	Ser	
283								225		230					235		240
284	Pro	Arg	Ser	Ala	Ala	Ser	Thr	Pro	Ala	Gly	Ser	Pro	Asp	Gly	Ser	Leu	
285								245		250					255		
286	Pro	Glu	His	His	Ala	Ala	Ala	Pro	Asn	Gly	Leu	Pro	Gly	Phe	Ser	Val	
287								260		265					270		
288	Glu	Asn	Ile	Met	Thr	Leu	Arg	Thr	Ser	Pro	Pro	Gly	Gly	Glu	Leu	Ser	

VERIFICATION SUMMARY
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:554 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:5, EXON LOCATION:
(1649)...(438)